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RAW SEQUENCE LISTING   DATE: 06/17/2002
PATENT APPLICATION: US/10/092,925   TIME: 12:40:29

Input Set : A:\06501-102US1.TXT
Output Set: N:\CRF3\06172002\J092925.raw

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  4  <110> APPLICANT: Kitamura, Toshio
  5        Morita, Sumiyo
  7  <120> TITLE OF INVENTION: TSG-LIKE GENE
 10  <130> FILE REFERENCE: 06501-102US1
 12  <140> CURRENT APPLICATION NUMBER: 10/092,925
 13  <141> CURRENT FILING DATE: 2002-06-10
 15  <150> PRIOR APPLICATION NUMBER: PCT/JP00/06050
 16  <151> PRIOR FILING DATE: 2000-09-06
 18  <150> PRIOR APPLICATION NUMBER: JP 11/252190
 19  <151> PRIOR FILING DATE: 1999-09-06
 21  <160> NUMBER OF SEQ ID NOS: 5
 23  <170> SOFTWARE: FastSEQ for Windows Version 4.0
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 28  <213> ORGANISM: Mus musculus
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 31  <221> NAME/KEY: CDS
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 36  ctactgagtg acttctttga agaacc atg aag tca cac tat att gtg cta gct     113
 37                                 Met Lys Ser His Tyr Ile Val Leu Ala
 38                                  1               5
 40  cta gcc tcc ctg acg ttc ctg ctg tgt ctc ccc gtg tcc cag agc tgt     161
 41  Leu Ala Ser Leu Thr Phe Leu Leu Cys Leu Pro Val Ser Gln Ser Cys
 42   10              15                  20                  25
 44  aac aaa gca ctc tgt gcc agc gat gtg agc aaa tgc ctc att cag gag     209
 45  Asn Lys Ala Leu Cys Ala Ser Asp Val Ser Lys Cys Leu Ile Gln Glu
 46               30                  35                  40
 48  ctc tgc cag tgc cgg cct gga gaa ggg aac tgc ccc tgc tgt aag gag     257
 49  Leu Cys Gln Cys Arg Pro Gly Glu Gly Asn Cys Pro Cys Cys Lys Glu
 50               45                  50                  55
 52  tgc atg ctg tgc ctc ggg gcc ctg tgg gac gag tgc tgc gac tgt gtc     305
 53  Cys Met Leu Cys Leu Gly Ala Leu Trp Asp Glu Cys Cys Asp Cys Val
 54           60                  65                  70
 56  ggt atg tgc aac cct cgg aat tac agc gac acc ccg ccc aca tcc aag     353
 57  Gly Met Cys Asn Pro Arg Asn Tyr Ser Asp Thr Pro Pro Thr Ser Lys
 58       75                  80                  85
 60  agc acc gtg gag gag ctg cac gag ccc att ccg tcc ctg ttc agg gcg     401
 61  Ser Thr Val Glu Glu Leu His Glu Pro Ile Pro Ser Leu Phe Arg Ala
 62   90                  95                  100                 105
 64  ctg acg gag ggc gac acc cag ctg aac tgg aac atc gtc tcc ttc cct     449
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65 Leu Thr Glu Gly Asp Thr Gln Leu Asn Trp Asn Ile Val Ser Phe Pro
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68 gtg gca gag gag ctg tca cac cat gaa aac cta gtc tcc ttc cta gaa   497
69 Val Ala Glu Glu Leu Ser His His Glu Asn Leu Val Ser Phe Leu Glu
70            125              130               135
72 act gtg aac cag ctg cac cac caa aac gtg tct gtt ccc agc aac aat   545
73 Thr Val Asn Gln Leu His His Gln Asn Val Ser Val Pro Ser Asn Asn
74            140              145               150
76 gtc cac gcc ccc ttc ccc agc gac aaa gag cgc atg tgc aca gtg gtt   593
77 Val His Ala Pro Phe Pro Ser Asp Lys Glu Arg Met Cys Thr Val Val
78            155              160               165
80 tac ttt gat gac tgc atg tcc atc cac cag tgt aag ata tcc tgc gaa   641
81 Tyr Phe Asp Asp Cys Met Ser Ile His Gln Cys Lys Ile Ser Cys Glu
82 170              175              180               185
84 tcc atg ggt gca tcc aag tat cgc tgg ttt cac aac gcc tgc tgc gag   689
85 Ser Met Gly Ala Ser Lys Tyr Arg Trp Phe His Asn Ala Cys Cys Glu
86            190              195               200
88 tgc atc ggt cca gag tgc att gac tat ggg agt aaa act gtc aag tgt   737
89 Cys Ile Gly Pro Glu Cys Ile Asp Tyr Gly Ser Lys Thr Val Lys Cys
90            205              210               215
92 atg aac tgc atg ttt taaagagggg gaagaaatgc aaaccaaagc agtaagtcat   792
93 Met Asn Cys Met Phe
94            220
96 gaagtgtgca gaaatcttgg ttctggtatg ctaggagtgt gttaagttat atgattgtaa   852
97 ctgtgctttt tatatctggt gcctattagt gtaggtcttt tccattggat tcaatggaac   912
98 tttagtcaca tgaggatcgg gagttcagag gagtcctggg aaaacctgac atgctgacag   972
99 aaggtgccgt cttcttccag ctttccaaac acttctcgtt ttgaacgtga tagcacaagc  1032
100 ctggtacatg tgtggttctc acctgccagt tgtagaacac taggtcccta tagtcacaca  1092
101 tctcttaatt gtgccttggc tggcttacct gttttgtatg agtaaatatt acagtttata  1152
102 attctaacaa ctcacattca agccatgctg aaacttaatt tcaaaccact ttacattggt  1212
103 tttagaaagt aaatatttac tatattttac aacagaagag ttttgcctag ggccagcgag  1272
104 ctgactcagt ggataaaggc gcttgctacc aagcctgata acctgagttc catccccaga  1332
105 gcccgtacag tggaaggaca ggaccagctg ctgggagttg tcctctgacc tccagacagg  1392
106 cacagtatca tgcgtggagg tgtgcttgtg tgtgcacaca cataactaac tgtttttaaa  1452
107 aatataaacc tcttacatgg tgaaatctaa atctgtcgtg tagctctcac actgacagtg  1512
108 gtttggatgt tatgtcccct gtccgcctgt agtgctggtg tggtgagaca cagagtcgtc  1572
109 actgctctgg tatagaagag ttttgtctac caagagtgtc atggcatacc tttggaactt  1632
110 catcaaatgc acttgaggat gacctgggtc aggaagtagc caggtaaaag cagcgggact  1692
111 gtaggcgatg ctccattaga ctccgtgcag agcagcaggt gcacagcata gctgggtgtg  1752
112 cggctgacca ggagagggtc tgactccgca ccagcagaac agcagggtct ccagcacgtg  1812
113 tgggaagcac gtgggagagg gttgaggaag gatgcacaga tgtggacaga gaagcataaa  1872
114 aatgtcggga actcctagta gggtccacct taaaatcgct ttatagtctc tggctttgtt  1932
115 actctgtaag attacacttg tttctggata tctgaatcca ataagcatc atatttaag   1992
116 aagctctgtt tctgaacttc caggggaaa tctgtttaat gtgtttactc ctagcatact  2052
117 acagaatttt ctagctctat agcttcttac ctagcgtttc catagtgctg agcttcatta  2112
118 ctacacgccc ttcctagtaa taaaattctc accttcaagc atgaatcaaa aacaaatatc  2172
119 tataatacac aggttcaatt ttatagaatt gctattttct ctagtgcata tctcattaaa  2232
120 agtaactttt taggaataat ctttatatgg gtacatattt tggtacataa aatagaaat   2292
121 gttcttaaac tcattttgta ttatttgaat agttacaaga tgatttgtgg tatcatgggt  2352
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122 acccattata aaccatgctc ttcccagtag ctgacgaact caaggtatca cagccttcta - 2412
123 agaagccgac ttagaacatg gctgtacatg aatattatac attaaggtgt cctctcactt   2472
124 ctacccagag tgcctctgtt caaaggtgcc ttggaaacat ttcagcccct tccttcttag   2532
125 ctcccacagg gctgtgggtg ttcttgaaat caggaggcgt tttgaaggac cacagctgct   2592
126 ccatttcagc cgctgattct taggaaagtt catgctctga cagaagtgtg ctttgatggc   2652
127 ttctagcggt gcatctcgtc tcgttttctt tgtttgtttt tgttgttgct atcatggttt   2712
128 ggtttggttt tgagacagga tctctgtgca gccctggctg gcctggaatg tactatgtag   2772
129 accaggctgg ctctcctcat gttttcttag tgatggccat aaacattgtt aaaatacatc   2832
130 accatctttt aaaaactttt cattattaaa atttaaaata tagcatgtca ttttttttacc  2892
131 ccatacattt gctatgaaaa attttttaaa ccacctgctt taactttttt attgccctgt   2952
132 ttttcctatt agaattgatc cccactgagg taaatttat aatcatgttt tgtgtatttt    3012
133 tcctggctcg ccaaggctta tgaagaaata gcagccattc cctgacaggt ttgcgctccc   3072
134 accacagaga ggctgagcaa gatgatcaga ggatcaaggc cagccagagc aaggcactgc   3132
135 ccagaaagca caagtcctgt gctcagcgtt ttgcgtagcg ttttattcct aattgaaatg   3192
136 taatatttca gaagctagca gcctcgctca gtctagacct tccacaccaa tctagcagcg   3252
137 attctcccgt actaaagcct ttgtaagagt ttacggttct tcctcagtga aaaatgatct   3312
138 tgttttttctt acagccggat ccaaagacgc tagatgttaa gggctgaggc tgaagcccgg  3372
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143 gagtagaatg tactgttcac acagcgtgtt gtgaaagggg tcctcacacc aaagtttaac   3672
144 tgtaaagttt agaaaaataa cattgtcatt agcatatttg aacacatatt tggaatttct   3732
145 aaaaagcatc aaaatagaaa aagaaagtga aactctggag aatgagatgc tgaagatggg   3792
146 ctatgattta aaggtctgtt ctgtagttag aaagcacctt ttaaagactt tgttcattcc   3852
147 caagagtcta tgttgattgc atttaacatg accgacaact tatatatgta attgtgtaca   3912
148 ttttcattgg ttgtctctgt agtccaaaag aaggtatttt aataaaaaat agaaatgact   3972
149 gtgaaaaaaa aaaa                                                      3986
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152 <211> LENGTH: 222
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159 Leu Cys Leu Pro Val Ser Gln Ser Cys Asn Lys Ala Leu Cys Ala Ser
160             20              25              30
161 Asp Val Ser Lys Cys Leu Ile Gln Glu Leu Cys Gln Cys Arg Pro Gly
162         35              40              45
163 Glu Gly Asn Cys Pro Cys Cys Lys Glu Cys Met Leu Cys Leu Gly Ala
164     50              55              60
165 Leu Trp Asp Glu Cys Cys Asp Cys Val Gly Met Cys Asn Pro Arg Asn
166 65              70              75              80
167 Tyr Ser Asp Thr Pro Pro Thr Ser Lys Ser Thr Val Glu Glu Leu His
168             85              90              95
169 Glu Pro Ile Pro Ser Leu Phe Arg Ala Leu Thr Glu Gly Asp Thr Gln
170             100             105             110
171 Leu Asn Trp Asn Ile Val Ser Phe Pro Val Ala Glu Glu Leu Ser His
172         115             120             125
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173 His Glu Asn Leu Val Ser Phe Leu Glu Thr Val Asn Gln Leu His His
174      130                 135                 140
175 Gln Asn Val Ser Val Pro Ser Asn Asn Val His Ala Pro Phe Pro Ser
176 145                 150                 155                 160
177 Asp Lys Glu Arg Met Cys Thr Val Val Tyr Phe Asp Asp Cys Met Ser
178                 165                 170                 175
179 Ile His Gln Cys Lys Ile Ser Cys Glu Ser Met Gly Ala Ser Lys Tyr
180                 180                 185                 190
181 Arg Trp Phe His Asn Ala Cys Cys Glu Cys Ile Gly Pro Glu Cys Ile
182         195                 200                 205
183 Asp Tyr Gly Ser Lys Thr Val Lys Cys Met Asn Cys Met Phe
184      210                 215                 220
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188 <212> TYPE: DNA
189 <213> ORGANISM: Artificial Sequence
191 <220> FEATURE:
192 <223> OTHER INFORMATION: Artificially Synthesized Primer Sequence
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196 gggggtggac catcctcta                                               19
198 <210> SEQ ID NO: 4
199 <211> LENGTH: 20
200 <212> TYPE: DNA
201 <213> ORGANISM: Artificial Sequence
203 <220> FEATURE:
204 <223> OTHER INFORMATION: Artificially Synthesized Primer Sequence
207 <400> SEQUENCE: 4
208 cgcgcagctg taaacggtag                                              20
210 <210> SEQ ID NO: 5
211 <211> LENGTH: 225
212 <212> TYPE: PRT
213 <213> ORGANISM: Drosophila melanogaster
215 <400> SEQUENCE: 5
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217 1                 5                 10                 15
218 Trp Ser Ser Leu Ala Asn Asp Asp Gly Cys Asn Glu Val Val Cys Gly
219                 20                 25                 30
220 Ser Val Val Ser Lys Cys Leu Ile Thr Gln Ser Cys Gln Cys Lys Leu
221         35                 40                 45
222 Asn Asp Cys His Cys Cys Lys Asp Cys Leu Asn Cys Leu Gly Glu Leu
223      50                 55                 60
224 Tyr Ile Glu Cys Cys Gly Cys Leu Asp Met Cys Pro Lys His Lys Asp
225 65                 70                 75                 80
226 Val Leu Pro Ser Leu Thr Pro Arg Ser Glu Ile Gly Asp Ile Glu Gly
227                 85                 90                 95
228 Val Pro Glu Leu Phe Asp Thr Leu Thr Ala Glu Asp Asp Glu Gly Trp
229                 100                 105                 110
230 Ser Thr Ile Arg Phe Ser Met Arg Ala Gly Phe Lys Gln Arg Val Gln
231         115                 120                 125
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RAW SEQUENCE LISTING   DATE: 06/17/2002
PATENT APPLICATION: US/10/092,925   TIME: 12:40:29

Input Set : A:\06501-102US1.TXT
Output Set: N:\CRF3\06172002\J092925.raw

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232 Gly Gly Ala Ser Gly Asp Ala Gly Asn Gly Asn Gly Asn Gly Asn Ala
233     130             135             140
234 Gly Ser Ala Gly Val Thr Leu Cys Thr Val Ile Tyr Val Asn Ser Cys
235 145             150             155             160
236 Ile Arg Ala Asn Lys Cys Arg Gln Gln Cys Glu Ser Met Gly Ala Ser
237             165             170             175
238 Ser Tyr Arg Trp Phe His Asp Gly Cys Cys Glu Cys Val Gly Glu Asn
239             180             185             190
240 Cys Leu Asn Tyr Gly Ile Asn Glu Ser Arg Cys Arg Gly Cys Pro Glu
241         195             200             205
242 Asp Gln Asp Gln Leu Leu Thr Ala Asp Thr Val Pro Ala Glu Ala Glu
243         210             215             220
244 Gln
245 225
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VERIFICATION SUMMARY   DATE: 06/17/2002
PATENT APPLICATION: US/10/092,925   TIME: 12:40:30

Input Set : A:\06501-102US1.TXT
Output Set: N:\CRF3\06172002\J092925.raw

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date